

SEQUENCE LISTING

<110> MIYAWAKI, ATSUSHI
 KOGURE, TAKAKO
 HAMA, HIROSHI
 KINJO, MASATAKA
 SAITO, KENTA
 KARASAWA, SATOSHI
 ARAKI, TOSHIO

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<141> 2006-06-02

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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
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Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	
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Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	
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aag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	tta	gtg	tca	cac	gtg	ttc	192
Lys	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	
	50					55				60						
tgt	tac	ggc	cac	aga	cct	ttt	act	aaa	tat	cca	gaa	gag	ata	cca	gac	240
Cys	Tyr	Gly	His	Arg	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	
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Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	
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 115 120 125
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
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 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
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 Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
 180 185 190
 cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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 35 40 45
 Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp
 145 150 155 160
 Thr Leu Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met
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 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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 20 25 30
 aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
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 tgc tac ggc cac aga tgt ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

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gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	agt	gcg	cat	ata	agc	ctt	336
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	
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Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	
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Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	
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Thr	Leu	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Met	
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Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Lys	Ile	Leu	Lys	Met	Pro	Gly	Ser	
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Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	
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Lys	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	
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Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
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Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Met
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Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Lys	Ile	Leu	Lys	Met	Pro	Gly	Ser
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Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	
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Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	
		35				40						45				
aag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	tta	gtg	tca	cac	gtg	ttc	192
Lys	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110

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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125

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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp
145 150 155 160

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa atg 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met
165 170 175

aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
180 185 190

cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
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 85 90 95
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
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Ala Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
                      85                      90                      95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
                      100                      105                      110

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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
                      115                      120                      125

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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145                      150                      155                      160

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
                      165                      170                      175

aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
                      180                      185                      190

cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
                      195                      200                      205

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 Cys Tyr Gly His Lys Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
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 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
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 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
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 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
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 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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 Glu Leu Val Glu Asp Ala Val Ala His Ser
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Cys Tyr Gly His Lys Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
      65                      70                      75

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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
      85                      90                      95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
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      100                      105                      110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
      115                      120                      125

cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
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Trp Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
      145                      150                      155

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
      165                      170                      175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
      180                      185                      190

cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
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 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 Cys Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
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 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 12
 <211> 657
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 <213> Fungia sp.

<220>
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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly	
20 25 30	
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc	144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala	
35 40 45	
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc	192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	
50 55 60	
tgt tac ggc cac aga ggt ttt act aaa tat cca gaa gag ata cca gac	240
Cys Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp	
65 70 75 80	
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe	
165 170 175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac	576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp	
180 185 190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr	
195 200 205	
gag ctg gta gaa gat gca gta gct cat tcc taa	657
Glu Leu Val Glu Asp Ala Val Ala His Ser	
210 215	

<210> 13

<211> 218

<212> PRT

<213> Fungia sp.

<400> 13

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Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
			20					25					30		
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
		35					40					45			
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
	50					55					60				
Cys	Tyr	Gly	His	Arg	Ala	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
65					70					75					80
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
			85						90					95	
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
			100					105					110		
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
		115					120					125			
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
	130					135					140				
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
145					150					155					160
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
				165					170					175	
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
			180					185					190		
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr
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<211> 657

<212> DNA

<213> Fungia sp.

<220>

<221> CDS

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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly	
20 25 30	
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc	144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala	
35 40 45	
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc	192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	
50 55 60	
tgt tac ggc cac aga gct ttt act aaa tat cca gaa gag ata cca gac	240
Cys Tyr Gly His Arg Ala Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp	
65 70 75 80	
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe	
165 170 175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac	576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp	
180 185 190	
cat tac atc ggg cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr	
195 200 205	
gag ctg gta gaa gat gca gta gct cat tcc taa	657
Glu Leu Val Glu Asp Ala Val Ala His Ser	
210 215	

<210> 15
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 <212> PRT
 <213> Fungia sp.

<400> 15

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			20					25					30		
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
		35					40					45			
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
	50					55					60				
Cys	Tyr	Gly	His	Arg	Ser	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
65					70					75				80	
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
			85						90					95	
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
			100					105					110		
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
		115					120					125			
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
	130					135					140				
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
145				150						155				160	
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
			165					170						175	
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
			180					185					190		
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr
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 <213> Fungia sp.

<220>

<221> CDS

<222> (1)..(654)

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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly	
20 25 30	
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc	144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala	
35 40 45	
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc	192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	
50 55 60	
tgt tac ggc cac aga tct ttt act aaa tat cca gaa gag ata cca gac	240
Cys Tyr Gly His Arg Ser Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp	
65 70 75 80	
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe	
165 170 175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac	576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp	
180 185 190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr	
195 200 205	

gag ctg gta gaa gat gca gta gct cat tcc taa
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

657

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 <213> Fungia sp.

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 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 18
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 <212> DNA
 <213> *Fungia* sp.

<220>
 <221> CDS
 <222> (1)..(654)

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ggc	tcc	gtc	aat	ggg	cat	gag	ttc	aca	att	gaa	ggg	gaa	ggc	aca	ggc	96
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	
			20					25					30			
aga	cct	tac	gag	gga	cat	caa	gag	atg	aca	cta	cgc	gtc	aca	atg	gcc	144
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	
		35					40					45				
gag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	tta	gtg	tca	cac	gtg	ttc	192
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	
	50					55					60					
tgt	tac	ggc	cac	aga	tgt	ttt	act	aaa	tat	cca	gaa	gag	ata	cca	gac	240
Cys	Tyr	Gly	His	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	
65					70					75					80	
tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	tca	tgg	gaa	agg	tcg	ttg	288
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	
			85						90					95		
gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	agt	gcg	cat	ata	agc	ctt	336
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	
			100					105					110			
aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	ttt	act	ggg	ggt	aac	ttt	384
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	
		115					120					125				
cct	gcc	gat	ggg	cct	atc	atg	caa	aac	caa	agt	ggt	gat	tgg	gag	cca	432
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	
	130					135					140					
tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	ggt	ctg	aag	ggg	gat	ggt	480
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	
145				150						155				160		
acg	atg	tac	cta	aaa	ctt	gaa	gga	ggc	ggc	aat	cac	aaa	tgc	caa	ttc	528
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe	
				165				170						175		
aag	act	act	tac	aag	gcg	gca	aaa	gag	att	ctt	gaa	atg	cca	gga	gac	576
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp	
			180					185						190		

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 19
 <211> 218
 <212> PRT
 <213> Fungia sp.

<400> 19
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 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
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 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 Cys Tyr Gly His Arg Thr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 20
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 <213> Fungia sp.

<220>
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 <222> (1)..(654)

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1				5					10					15		
ggc	tcc	gtc	aat	ggg	cat	gag	ttc	aca	att	gaa	ggg	gaa	ggc	aca	ggc	96
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	
			20					25					30			
aga	cct	tac	gag	gga	cat	caa	gag	atg	aca	cta	cgc	gtc	aca	atg	gcc	144
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	
		35					40					45				
gag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	tta	gtg	tca	cac	gtg	ttc	192
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	
	50					55					60					
tgt	tac	ggc	cac	aga	act	ttt	act	aaa	tat	cca	gaa	gag	ata	cca	gac	240
Cys	Tyr	Gly	His	Arg	Thr	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	
65					70					75				80		
tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	tca	tgg	gaa	agg	tcg	ttg	288
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	
			85						90					95		
gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	agt	gcg	cat	ata	agc	ctt	336
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	
			100					105					110			
aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	ttt	act	ggg	gtt	aac	ttt	384
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	
		115					120					125				
cct	gcc	gat	ggg	cct	atc	atg	caa	aac	caa	agt	gtt	gat	tgg	gag	cca	432
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	
	130					135					140					
tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	gtt	ctg	aag	ggg	gat	gtt	480
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	
145					150					155					160	
acg	atg	tac	cta	aaa	ctt	gaa	gga	ggc	ggc	aat	cac	aaa	tgc	caa	ttc	528
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe	
				165				170						175		
aag	act	act	tac	aag	gcg	gca	aaa	gag	att	ctt	gaa	atg	cca	gga	gac	576
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp	
			180					185					190			

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 21
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 <212> PRT
 <213> Fungia sp.

<400> 21
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1 5 10 15
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 Cys Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 22
 <211> 657
 <212> DNA
 <213> *Fungia* sp.

<220>
 <221> CDS
 <222> (1)..(654)

<400> 22

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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp	
1 5 10 15	
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc	96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly	
20 25 30	
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc	144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala	
35 40 45	
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc	192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	
50 55 60	
tgt tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac	240
Cys Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp	
65 70 75 80	
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe	
165 170 175	

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 23

<211> 218

<212> PRT

<213> *Fungia* sp.

<400> 23

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1 5 10 15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

Cys Tyr Gly His Arg Leu Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 24
 <211> 657
 <212> DNA
 <213> *Fungia* sp.

<220>
 <221> CDS
 <222> (1)..(654)

<400> 24

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1				5					10					15		
ggc	tcc	gtc	aat	ggg	cat	gag	ttc	aca	att	gaa	ggg	gaa	ggc	aca	ggc	96
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	
			20					25					30			
aga	cct	tac	gag	gga	cat	caa	gag	atg	aca	cta	cgc	gtc	aca	atg	gcc	144
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	
		35					40					45				
gag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	tta	gtg	tca	cac	gtg	ttc	192
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	
	50					55					60					
tgt	tac	ggc	cac	aga	ctt	ttt	act	aaa	tat	cca	gaa	gag	ata	cca	gac	240
Cys	Tyr	Gly	His	Arg	Leu	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	
65					70					75				80		
tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	tca	tgg	gaa	agg	tcg	ttg	288
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	
			85						90					95		
gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	agt	gcg	cat	ata	agc	ctt	336
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	
			100				105						110			
aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	ttt	act	ggg	ggt	aac	ttt	384
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	
		115					120					125				
cct	gcc	gat	ggg	cct	atc	atg	caa	aac	caa	agt	ggt	gat	tgg	gag	cca	432
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	
	130					135					140					
tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	ggt	ctg	aag	ggg	gat	ggt	480
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	
145					150					155					160	

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 25

<211> 218

<212> PRT

<213> Fungia sp.

<400> 25

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 20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

Cys Tyr Gly His Arg Tyr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 26
 <211> 657
 <212> DNA
 <213> Fungia sp.

<220>
 <221> CDS
 <222> (1)..(654)

<400> 26
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 1 5 10 15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

tgt tac ggc cac aga tac ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Tyr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 27
 <211> 218
 <212> PRT
 <213> Fungia sp.

<400> 27
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 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 Cys Tyr Gly His Arg Gln Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160

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<220>  
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<400> 28																	
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1				5				10				15					
ggc	tcc	gtc	aat	ggg	cat	gag	ttc	aca	att	gaa	ggt	gaa	ggc	aca	ggc	96	
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly		
				20				25				30					
aga	cct	tac	gag	gga	cat	caa	gag	atg	aca	cta	cgc	gtc	aca	atg	gcc	144	
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala		
35				40				45									
gag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	tta	gtg	tca	cac	gtg	ttc	192	
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe		
50				55				60									
tgt	tac	ggc	cac	aga	cag	ttt	act	aaa	tat	cca	gaa	gag	ata	cca	gac	240	
Cys	Tyr	Gly	His	Arg	Gln	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp		
65				70				75				80					
tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	tca	tgg	gaa	agg	tcg	ttg	288	
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu		
				85				90				95					
gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	agt	gcg	cat	ata	agc	ctt	336	
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu		
100				105				110									
aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	ttt	act	ggg	gtt	aac	ttt	384	
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe		
115				120				125									

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cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
    130                      135                      140

tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
    145                      150                      155                      160

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Phe
                      165                      170                      175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
                      180                      185                      190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
    195                      200                      205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
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<210> 29
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 <212> PRT
 <213> *Fungia* sp.

<220>
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    20                      25                      30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
    35                      40                      45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
    50                      55                      60

Cys Tyr Gly His Arg Asn Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
    65                      70                      75                      80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
    85                      90                      95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
    100                      105                      110

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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Xaa Leu Glu Met Pro Gly Asp
 180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 30
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 <212> DNA
 <213> Fungia sp.

<220>
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 <222> (1)..(654)

<220>
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 <223> a, c, g, t, unknown or other

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 1 5 10 15

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 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

tgt tac ggc cac aga aat ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Asn Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe	
165 170 175	
aag act act tac aag gcg gca aaa gag ntt ctt gaa atg cca gga gac	576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Xaa Leu Glu Met Pro Gly Asp	
180 185 190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr	
195 200 205	
gag ctg gta gaa gat gca gta gct cat tcc taa	657
Glu Leu Val Glu Asp Ala Val Ala His Ser	
210 215	

<210> 31

<211> 665

<212> PRT

<213> Fungia sp.

<400> 31

Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly	
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20 25 30	
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35 40 45	
Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser	
50 55 60	
Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val	
65 70 75 80	

Asp	Glu	Gly	Ala	Pro 85	Gly	Lys	Gln	Ala	Ala	Ala	Gln	Pro	His	Thr	Glu
Ile	Pro	Glu	Gly 100	Thr	Thr	Ala	Glu	Glu 105	Ala	Gly	Ile	Gly	Asp 110	Thr	Pro
Ser	Leu	Glu 115	Asp	Glu	Ala	Ala	Gly 120	His	Val	Thr	Gln	Ala 125	Arg	Met	Val
Ser	Lys 130	Ser	Lys	Asp	Gly	Thr 135	Gly	Ser	Asp	Asp	Lys 140	Lys	Ala	Lys	Gly
Ala 145	Asp	Gly	Lys	Thr	Lys 150	Ile	Ala	Thr	Pro	Arg 155	Gly	Ala	Ala	Pro	Pro 160
Gly	Gln	Lys	Gly	Gln 165	Ala	Asn	Ala	Thr	Arg 170	Ile	Pro	Ala	Lys	Thr 175	Pro
Pro	Ala	Pro	Lys 180	Thr	Pro	Pro	Ser	Ser 185	Gly	Glu	Pro	Pro	Lys 190	Ser	Gly
Asp	Arg	Ser 195	Gly	Tyr	Ser	Ser	Pro 200	Gly	Ser	Pro	Gly	Thr 205	Pro	Gly	Ser
Arg	Ser 210	Arg	Thr	Pro	Ser	Leu 215	Pro	Thr	Pro	Pro	Thr 220	Arg	Glu	Pro	Lys
Lys 225	Val	Ala	Val	Val	Arg 230	Thr	Pro	Pro	Lys	Ser 235	Pro	Ser	Ser	Ala	Lys 240
Ser	Arg	Leu	Gln 245	Thr	Ala	Pro	Val	Pro	Met 250	Pro	Asp	Leu	Lys	Asn 255	Val
Lys	Ser	Lys	Ile 260	Gly	Ser	Thr	Glu	Asn 265	Leu	Lys	His	Gln 270	Pro	Gly	Gly
Gly	Lys	Val 275	Gln	Ile	Ile	Asn	Lys 280	Lys	Leu	Asp	Leu	Ser 285	Asn	Val	Gln
Ser	Lys 290	Cys	Gly	Ser	Lys	Asp 295	Asn	Ile	Lys	His	Val 300	Pro	Gly	Gly	Gly
Ser 305	Val	Gln	Ile	Val	Tyr 310	Lys	Pro	Val	Asp	Leu 315	Ser	Lys	Val	Thr	Ser 320
Lys	Cys	Gly	Ser	Leu 325	Gly	Asn	Ile	His	His 330	Lys	Pro	Gly	Gly	Gly 335	Gln
Val	Glu	Val	Lys 340	Ser	Glu	Lys	Leu	Asp 345	Phe	Lys	Asp	Arg	Val 350	Gln	Ser
Lys	Ile	Gly 355	Ser	Leu	Asp	Asn	Ile 360	Thr	His	Val	Pro	Gly 365	Gly	Gly	Asn
Lys	Lys 370	Ile	Glu	Thr	His	Lys 375	Leu	Thr	Phe	Arg	Glu 380	Asn	Ala	Lys	Ala

Lys	Thr	Asp	His	Gly	Ala	Glu	Ile	Val	Tyr	Lys	Ser	Pro	Val	Val	Ser	385	390	395	400
Gly	Asp	Thr	Ser	Pro	Arg	His	Leu	Ser	Asn	Val	Ser	Ser	Thr	Gly	Ser	405	410	415	
Ile	Asp	Met	Val	Asp	Ser	Pro	Gln	Leu	Ala	Thr	Leu	Ala	Asp	Glu	Val	420	425	430	
Ser	Ala	Ser	Leu	Ala	Lys	Gln	Gly	Leu	Gly	Ser	Gly	Gly	Glu	Phe	Met	435	440	445	
Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	Met	Arg	Tyr	Tyr	Met	Asp	Gly	450	455	460	
Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	Arg	465	470	475	480
Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	Glu	485	490	495	
Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	Cys	500	505	510	
Tyr	Gly	His	Arg	Val	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	Tyr	515	520	525	
Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	Glu	530	535	540	
Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	Arg	545	550	555	560
Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	Pro	565	570	575	
Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	Ser	580	585	590	
Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	Thr	595	600	605	
Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe	Lys	610	615	620	
Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp	His	625	630	635	640
Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr	Glu	645	650	655	
Leu	Val	Glu	Asp	Ala	Val	Ala	His	Ser								660	665		

<210> 32
 <211> 1998
 <212> DNA
 <213> *Fungia* sp.

<220>
 <221> CDS
 <222> (1)..(1995)

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acg tac ggg ttg ggg gac agg aaa gat cag ggg ggc tac acc atg cac	96
Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His	
20 25 30	
caa gac caa gag ggt gac acg gac gct ggc ctg aaa gaa tct ccc ctg	144
Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu	
35 40 45	
cag acc ccc act gag gac gga tct gag gaa ccg ggc tct gaa acc tct	192
Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser	
50 55 60	
gat gct aag agc act cca aca gcg gaa gat gtg aca gca ccc tta gtg	240
Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val	
65 70 75 80	
gat gag gga gct ccc ggc aag cag gct gcc gcg cag ccc cac acg gag	288
Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu	
85 90 95	
atc cca gaa gga acc aca gct gaa gaa gca ggc att gga gac acc ccc	336
Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro	
100 105 110	
agc ctg gaa gac gaa gct gct ggt cac gtg acc caa gct cgc atg gtc	384
Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val	
115 120 125	
agt aaa agc aaa gac ggg act gga agc gat gac aaa aaa gcc aag ggg	432
Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly	
130 135 140	
gct gat ggt aaa acg aag atc gcc aca ccg cgg gga gca gcc cct cca	480
Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro	
145 150 155 160	
ggc cag aag ggc cag gcc aac gcc acc agg att cca gca aaa acc ccg	528
Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro	
165 170 175	
ccc gct cca aag aca cca ccc agc tct ggt gaa cct cca aaa tca ggg	576
Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly	
180 185 190	

gat	cgc	agc	ggc	tac	agc	agc	ccc	ggc	tcc	cca	ggc	act	ccc	ggc	agc	624
Asp	Arg	Ser	Gly	Tyr	Ser	Ser	Pro	Gly	Ser	Pro	Gly	Thr	Pro	Gly	Ser	
		195					200					205				
cgc	tcc	cgc	acc	ccg	tcc	ctt	cca	acc	cca	ccc	acc	cgg	gag	ccc	aag	672
Arg	Ser	Arg	Thr	Pro	Ser	Leu	Pro	Thr	Pro	Pro	Thr	Arg	Glu	Pro	Lys	
	210					215					220					
aag	gtg	gca	gtg	gtc	cgt	act	cca	ccc	aag	tcg	ccg	tct	tcc	gcc	aag	720
Lys	Val	Ala	Val	Val	Arg	Thr	Pro	Pro	Lys	Ser	Pro	Ser	Ser	Ala	Lys	
225					230				235						240	
agc	cgc	ctg	cag	aca	gcc	ccc	gtg	ccc	atg	cca	gac	ctg	aag	aat	gtc	768
Ser	Arg	Leu	Gln	Thr	Ala	Pro	Val	Pro	Met	Pro	Asp	Leu	Lys	Asn	Val	
			245						250					255		
aag	tcc	aag	atc	ggc	tcc	act	gag	aac	ctg	aag	cac	cag	ccg	gga	ggc	816
Lys	Ser	Lys	Ile	Gly	Ser	Thr	Glu	Asn	Leu	Lys	His	Gln	Pro	Gly	Gly	
			260					265					270			
ggg	aag	gtg	cag	ata	att	aat	aag	aag	ctg	gat	ctt	agc	aac	gtc	cag	864
Gly	Lys	Val	Gln	Ile	Ile	Asn	Lys	Lys	Leu	Asp	Leu	Ser	Asn	Val	Gln	
		275					280					285				
tcc	aag	tgt	ggc	tca	aag	gat	aat	atc	aaa	cac	gtc	ccg	gga	ggc	ggc	912
Ser	Lys	Cys	Gly	Ser	Lys	Asp	Asn	Ile	Lys	His	Val	Pro	Gly	Gly	Gly	
	290					295					300					
agt	gtg	caa	ata	gtc	tac	aaa	cca	gtt	gac	ctg	agc	aag	gtg	acc	tcc	960
Ser	Val	Gln	Ile	Val	Tyr	Lys	Pro	Val	Asp	Leu	Ser	Lys	Val	Thr	Ser	
305					310				315						320	
aag	tgt	ggc	tca	tta	ggc	aac	atc	cat	cat	aaa	cca	gga	ggt	ggc	cag	1008
Lys	Cys	Gly	Ser	Leu	Gly	Asn	Ile	His	His	Lys	Pro	Gly	Gly	Gly	Gln	
			325					330					335			
gtg	gaa	gta	aaa	tct	gag	aag	ctt	gac	ttc	aag	gac	aga	gtc	cag	tcg	1056
Val	Glu	Val	Lys	Ser	Glu	Lys	Leu	Asp	Phe	Lys	Asp	Arg	Val	Gln	Ser	
			340					345					350			
aag	att	ggg	tcc	ctg	gac	aat	atc	acc	cac	gtc	cct	ggc	gga	gga	aat	1104
Lys	Ile	Gly	Ser	Leu	Asp	Asn	Ile	Thr	His	Val	Pro	Gly	Gly	Gly	Asn	
		355				360						365				
aaa	aag	att	gaa	acc	cac	aag	ctg	acc	ttc	cgc	gag	aac	gcc	aaa	gcc	1152
Lys	Lys	Ile	Glu	Thr	His	Lys	Leu	Thr	Phe	Arg	Glu	Asn	Ala	Lys	Ala	
	370					375					380					
aag	aca	gac	cac	ggg	gcg	gag	atc	gtg	tac	aag	tcg	cca	gtg	gtg	tct	1200
Lys	Thr	Asp	His	Gly	Ala	Glu	Ile	Val	Tyr	Lys	Ser	Pro	Val	Val	Ser	
385					390					395					400	
ggg	gac	acg	tct	cca	cgg	cat	ctc	agc	aat	gtc	tcc	tcc	acc	ggc	agc	1248
Gly	Asp	Thr	Ser	Pro	Arg	His	Leu	Ser	Asn	Val	Ser	Ser	Thr	Gly	Ser	
				405					410					415		

atc gac atg gta gac tcg ccc cag ctc gcc acg cta gct gac gag gtg Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val 420 425 430	1296
tct gcc tcc ctg gcc aag cag ggt ttg gga tcc gga ggt gaa ttc atg Ser Ala Ser Leu Ala Lys Gln Gly Leu Gly Ser Gly Gly Glu Phe Met 435 440 445	1344
gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac ggc Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp Gly 450 455 460	1392
tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc aga Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly Arg 465 470 475 480	1440
cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc gag Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala Glu 485 490 495	1488
ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc tgt Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe Cys 500 505 510	1536
tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac tat Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp Tyr 515 520 525	1584
ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg gag Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu Glu 530 535 540	1632
ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt aga Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu Arg 545 550 555 560	1680
gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt cct Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe Pro 565 570 575	1728
gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca tca Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro Ser 580 585 590	1776
acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt acg Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val Thr 595 600 605	1824
atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc aag Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe Lys 610 615 620	1872
act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac cat Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp His 625 630 635 640	1920

tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act gag 1968
 Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr Glu
 645 650 655

ctg gta gaa gat gca gta gct cat tcc taa 1998
 Leu Val Glu Asp Ala Val Ala His Ser
 660 665

<210> 33
 <211> 480
 <212> PRT
 <213> Fungia sp.

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 Met Lys Ala Ala Pro Met Lys Glu Ala Asn Val His Gly Gln Gly Asn
 20 25 30
 Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn
 35 40 45
 Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp
 50 55 60
 Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val
 65 70 75 80
 Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg
 85 90 95
 Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu
 100 105 110
 Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg
 115 120 125
 Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys
 130 135 140
 Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val
 145 150 155 160
 Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser
 165 170 175
 Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met
 180 185 190
 Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn
 195 200 205
 Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp
 210 215 220

Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys
 225 230 235 240
 Val Cys Thr Leu Thr Ile Lys Arg Gly Arg Gly Val Pro Arg Ala Arg
 245 250 255
 Asp Pro Pro Val Ala Thr Met Val Ser Val Ile Lys Pro Glu Met Lys
 260 265 270
 Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile
 275 280 285
 Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr
 290 295 300
 Leu Arg Val Thr Met Ala Glu Gly Gly Pro Met Pro Phe Ala Phe Asp
 305 310 315 320
 Leu Val Ser His Val Phe Cys Tyr Gly His Arg Val Phe Thr Lys Tyr
 325 330 335
 Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu
 340 345 350
 Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val
 355 360 365
 Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys
 370 375 380
 Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln
 385 390 395 400
 Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
 405 410 415
 Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly
 420 425 430
 Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile
 435 440 445
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 Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
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<210> 34

<211> 1443

<212> DNA

<213> *Fungia* sp.

<220>

<221> CDS

<222> (1)..(1440)

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atg aag gct gcg ccc atg aaa gaa gca aac gtc cac gga caa ggc aac	96
Met Lys Ala Ala Pro Met Lys Glu Ala Asn Val His Gly Gln Gly Asn	
20 25 30	
ttg gcc tac cca gct gtg cgg acc cat ggg act ctg gag agc gtg aat	144
Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn	
35 40 45	
ggg ccc agg gca ggt tcg aga ggt ctg acg acg acg tcc ctg gct gac	192
Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp	
50 55 60	
act ttt gag cac gtg atc gaa gag ctg ctg gat gag gac cag aag gtt	240
Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val	
65 70 75 80	
cgg ccc aac gaa gaa aac cat aag gac gcg gac ttg tac act tcc cgg	288
Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg	
85 90 95	
gtg atg ctc agc agt caa gtg cct ttg gag cct cct ctg ctc ttt ctg	336
Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu	
100 105 110	
ctg gag gaa tac aaa aat tac ctg gat gcc gca aac atg tct atg agg	384
Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg	
115 120 125	
gtt cgg cgc cac tcc gac ccc gcc cgc cgt ggg gag ctg agc gtg tgt	432
Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys	
130 135 140	
gac agt att agc gag tgg gtc aca gcg gca gat aaa aag act gca gtg	480
Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val	
145 150 155 160	
gac atg tcc ggt ggg acg gtc aca gtc ctg gag aaa gtc ccg gta tca	528
Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser	
165 170 175	
aaa ggc caa ctg aag caa tat ttc tac gag acc aag tgt aat ccc atg	576
Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met	
180 185 190	
ggg tac acg aag gaa ggc tgc agg ggc ata gac aaa agg cac tgg aac	624
Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn	
195 200 205	

tcg	caa	tgc	cga	act	acc	caa	tcg	tat	gtt	cgg	gcc	ctt	act	atg	gat	672
Ser	Gln	Cys	Arg	Thr	Thr	Gln	Ser	Tyr	Val	Arg	Ala	Leu	Thr	Met	Asp	
210						215					220					
agc	aaa	aag	aga	att	ggc	tgg	cgg	ttc	ata	agg	ata	gac	act	tcc	tgt	720
Ser	Lys	Lys	Arg	Ile	Gly	Trp	Arg	Phe	Ile	Arg	Ile	Asp	Thr	Ser	Cys	
225					230					235					240	
gta	tgt	aca	ctg	acc	att	aaa	agg	gga	aga	ggg	gta	ccg	cgg	gcc	cgg	768
Val	Cys	Thr	Leu	Thr	Ile	Lys	Arg	Gly	Arg	Gly	Val	Pro	Arg	Ala	Arg	
				245				250						255		
gac	cca	ccg	gtc	gcc	acc	atg	gtg	agt	gtg	att	aaa	cca	gag	atg	aag	816
Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	
			260					265					270			
atg	agg	tac	tac	atg	gac	ggc	tcc	gtc	aat	ggg	cat	gag	ttc	aca	att	864
Met	Arg	Tyr	Tyr	Met	Asp	Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	
		275					280						285			
gaa	ggt	gaa	ggc	aca	ggc	aga	cct	tac	gag	gga	cat	caa	gag	atg	aca	912
Glu	Gly	Glu	Gly	Thr	Gly	Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	
290						295					300					
cta	cgc	gtc	aca	atg	gcc	gag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	960
Leu	Arg	Val	Thr	Met	Ala	Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	
305					310					315					320	
tta	gtg	tca	cac	gtg	ttc	tgt	tac	ggc	cac	aga	gta	ttt	act	aaa	tat	1008
Leu	Val	Ser	His	Val	Phe	Cys	Tyr	Gly	His	Arg	Val	Phe	Thr	Lys	Tyr	
				325					330					335		
cca	gaa	gag	ata	cca	gac	tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	1056
Pro	Glu	Glu	Ile	Pro	Asp	Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	
			340					345					350			
tca	tgg	gaa	agg	tcg	ttg	gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	1104
Ser	Trp	Glu	Arg	Ser	Leu	Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	
		355					360						365			
agt	gcg	cat	ata	agc	ctt	aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	1152
Ser	Ala	His	Ile	Ser	Leu	Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	
		370				375					380					
ttt	act	ggg	gtt	aac	ttt	cct	gcc	gat	ggg	cct	atc	atg	caa	aac	caa	1200
Phe	Thr	Gly	Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	
385					390					395					400	
agt	gtt	gat	tgg	gag	cca	tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	1248
Ser	Val	Asp	Trp	Glu	Pro	Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	
			405						410					415		
gtt	ctg	aag	ggg	gat	gtt	acg	atg	tac	cta	aaa	ctt	gaa	gga	ggc	ggc	1296
Val	Leu	Lys	Gly	Asp	Val	Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	
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<211> 464
<212> PRT
<213> Fungia sp.
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Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly
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Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val
          35          40          45
Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
  50          55          60
Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
  65          70          75          80
Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
          85          90          95
Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
          100          105          110
Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
          115          120          125
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
          130          135          140
Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
  145          150          155          160
Arg Gly Asp Val Thr Gln Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln
          165          170          175
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
          180          185          190

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Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
 195 200 205
 Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala
 210 215 220
 His Val Asn Pro Leu Lys Val Lys Gly Gly Ser Gly Gly Asp Glu Val
 225 230 235 240
 Asp Gly Thr Gly Gly Ser Met Val Ser Val Ile Lys Pro Glu Met Lys
 245 250 255
 Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile
 260 265 270
 Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr
 275 280 285
 Leu Arg Val Thr Met Ala Lys Gly Gly Pro Met Pro Phe Ala Phe Asp
 290 295 300
 Leu Val Ser His Val Phe Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr
 305 310 315 320
 Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu
 325 330 335
 Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val
 340 345 350
 Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys
 355 360 365
 Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln
 370 375 380
 Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
 385 390 395 400
 Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly
 405 410 415
 Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile
 420 425 430
 Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys
 435 440 445
 Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
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<210> 36
 <211> 1395
 <212> DNA
 <213> Fungia sp.

<220>

<221> CDS

<222> (1)..(1392)

<400> 36

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tac cgt atg gaa ggc agt gtc aat ggc cat gaa ttc acg atc gaa ggt	96
Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly	
20 25 30	
gta gga act gga aac cct tac gaa ggg aaa cag atg tcc gaa tta gtg	144
Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val	
35 40 45	
atc atc aag tct aag gga aaa ccc ctt cca ttc tcc ttt gac ata ctg	192
Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu	
50 55 60	
tca aca gcc ttt caa tat gga aac aga tgc ttc aca aag tac cct gca	240
Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala	
65 70 75 80	
gac atg cct gac tat ttc aag caa gca ttc cca gat gga atg tca tat	288
Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr	
85 90 95	
gaa agg tca ttt cta ttt gag gat gga gga gtt gct aca gcc agc tgg	336
Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp	
100 105 110	
agc att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc tat cat	384
Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His	
115 120 125	
ggc gta aac ttt ccc gct gat gga ccc gta atg aag aag cag aca att	432
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile	
130 135 140	
ggc tgg gat aag tcc ttc gaa aaa atg agt gtg gct aaa gag gtg cta	480
Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu	
145 150 155 160	
aga ggt gat gtg act cag ttt ctt ctg ctc gaa gga ggt ggt tac cag	528
Arg Gly Asp Val Thr Gln Phe Leu Leu Glu Gly Gly Gly Tyr Gln	
165 170 175	
aga tgc cgg ttt cac tcc act tac aaa acg gag aag cca gtc gca atg	576
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met	
180 185 190	
ccc ccg agt cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc	624
Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly	
195 200 205	

caa act gca aaa ggc ttc aag gtc aag ctg gaa gaa cat gct gag gct	672
Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala	
210 215 220	
cat gtt aac cct ttg aag gtt aaa ggt ggc agc ggt ggc gac gag gtg	720
His Val Asn Pro Leu Lys Val Lys Gly Gly Ser Gly Gly Asp Glu Val	
225 230 235 240	
gac ggt acc ggt ggc agc atg gtg agt gtg att aaa cca gag atg aag	768
Asp Gly Thr Gly Gly Ser Met Val Ser Val Ile Lys Pro Glu Met Lys	
245 250 255	
atg agg tac tac atg gac ggc tcc gtc aat ggg cat gag ttc aca att	816
Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile	
260 265 270	
gaa ggt gaa ggc aca ggc aga cct tac gag gga cat caa gag atg aca	864
Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr	
275 280 285	
cta cgc gtc aca atg gcc aag ggc ggg cca atg cct ttc gcg ttt gac	912
Leu Arg Val Thr Met Ala Lys Gly Gly Pro Met Pro Phe Ala Phe Asp	
290 295 300	
tta gtg tca cac gtg ttc tgt tac ggc cac aga cct ttt act aaa tat	960
Leu Val Ser His Val Phe Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr	
305 310 315 320	
cca gaa gag ata cca gac tat ttc aaa caa gca ttt cct gaa ggc ctg	1008
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu	
325 330 335	
tca tgg gaa agg tcg ttg gag ttc gaa gat ggt ggc tcc gct tca gtc	1056
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val	
340 345 350	
agt gcg cat ata agc ctt aga gga aac acc ttc tac cac aaa tcc aaa	1104
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys	
355 360 365	
ttt act ggg gtt aac ttt cct gcc gat ggt cct atc atg caa aac caa	1152
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln	
370 375 380	
agt gtt gat tgg gag cca tca acc gag aaa att act gcc agc gac gga	1200
Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly	
385 390 395 400	
gtt ctg aag ggt gat gtt acg atg tac cta aaa ctt gaa gga ggc ggc	1248
Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly	
405 410 415	
aat cac aaa tgc caa ttc aag act act tac aag gcg gca aaa aag att	1296
Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile	
420 425 430	

ctt aaa atg cca gga agc cat tac atc agc cat cgc ctc gtc agg aaa 1344
 Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys
 435 440 445

acc gaa ggc aac att act gag ctg gta gaa gat gca gta gct cat tcc 1392
Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
450 455 460

taa 1395

<210> 37

<211> 221

<212> PRT

<213> Montipora. sp

<400> 37

Met Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr Gly
50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met His Phe Glu
85 90 95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
100 105 110

Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro Asn
 . 115 120 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
130 135 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
145 150 155 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
165 170 175

Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp
180 185 190

Arg Lys Leu Asp Val Thr Ser His Asn Lys Asp Tyr Thr Phe Val Glu
195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 38
 <211> 666
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1)..(663)

<400> 38
 atg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg tca ggc 48
 Met Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
 1 5 10 15

acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag 96
 Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
 20 25 30

cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggt gga 144
 Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
 35 40 45

cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac gga 192
 Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr Gly
 50 55 60

agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag 240
 Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
 65 70 75 80

cag tca ttc cct gag gga tat aca tgg gag agg atc atg cac ttt gaa 288
 Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met His Phe Glu
 85 90 95

gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac 336
 Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
 100 105 110

tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc aat 384
 Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro Asn
 115 120 125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag 432
 Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
 130 135 140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct 480
 Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
 145 150 155 160

ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act 528
 Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
 165 170 175

tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt gac 576
 Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp
 180 185 190

cgc aaa ctg gat gta acc agt cac aac aag gat tac aca ttt gtt gag 624
 Arg Lys Leu Asp Val Thr Ser His Asn Lys Asp Tyr Thr Phe Val Glu
 195 200 205

cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 666
 Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 39

<211> 222

<212> PRT

<213> Montipora. sp

<400> 39

Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
 1 5 10 15

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
 20 25 30

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
 35 40 45

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr
 50 55 60

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
 65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe
 85 90 95

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
 100 105 110

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro
 115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140

Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met
 145 150 155 160

Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
 165 170 175

Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val
 180 185 190

Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205

Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 40

<211> 669

<212> DNA

<213> Montipora. sp

<220>

<221> CDS

<222> (1)..(666)

<400> 40

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 Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
 1 5 10 15

ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96
 Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
 20 25 30

aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144
 Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
 35 40 45

gga cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac 192
 Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr
 50 55 60

gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240
 Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
 65 70 75 80

aag cag tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttt 288
 Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe
 85 90 95

gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336
 Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
 100 105 110

aac tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc 384
 Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro
 115 120 125

aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140

gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat ttt atg 480
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met
 145 150 155 160

50

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gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct 528
Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
      165      170      175

act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt 576
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val
      180      185      190

gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
      195      200      205

gag cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 669
Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
      210      215      220

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<210> 41
 <211> 222
 <212> PRT
 <213> Montipora. sp

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<400> 41
Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
  1      5      10      15

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
      20      25      30

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
      35      40      45

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr
      50      55      60

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
      65      70      75      80

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe
      85      90      95

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
      100      105      110

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro
      115      120      125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
      130      135      140

Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met
      145      150      155      160

Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
      165      170      175

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Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile
 180 185 190

Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205

Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 42
 <211> 669
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1)..(666)

<400> 42

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Met	Val	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met	Ser	
1				5					10					15		
ggc	acg	gtc	aat	gga	cac	tac	ttt	gag	gtc	gaa	ggc	gat	gga	aaa	gga	96
Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	Gly	
			20					25					30			
aag	cct	tac	gag	gga	gag	cag	aca	gta	aag	ctc	act	gtc	acc	aag	ggc	144
Lys	Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	Gly	
		35					40					45				
gga	cct	ctg	cca	ttt	gct	tgg	gat	att	tta	tca	cca	ctg	ttt	cag	tac	192
Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Phe	Gln	Tyr	
	50					55					60					
gga	agc	ata	cca	ttc	acc	aag	tac	cct	gaa	gac	atc	cct	gat	tat	gta	240
Gly	Ser	Ile	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Val	
	65				70				75						80	
aag	cag	tca	ttc	cct	gag	gga	tat	aca	tgg	gag	agg	acc	atg	aac	ttt	288
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Thr	Met	Asn	Phe	
			85						90					95		
gaa	gat	ggc	gca	gtg	tgt	act	gtc	agc	aat	gat	tcc	agc	atc	caa	ggc	336
Glu	Asp	Gly	Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln	Gly	
			100					105					110			
aac	tgt	ttc	atc	tac	aat	gtc	aaa	atc	tct	ggc	acg	aac	ttt	cct	ccc	384
Asn	Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Pro	Pro	
		115					120					125				
aat	gga	cct	gtt	atg	cag	aag	aag	aca	cag	ggc	tgg	gaa	ccc	agc	act	432
Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser	Thr	
	130					135					140					

gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat atg 480
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met
 145 150 155 160

gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct 528
 Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
 165 170 175

act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat att 576
 Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile
 180 185 190

gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624
 Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205

gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tga 669
 Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 43

<211> 222

<212> PRT

<213> Montipora. sp

<400> 43

Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
 1 5 10 15

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
 20 25 30

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
 35 40 45

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Met Cys Tyr
 50 55 60

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
 65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe
 85 90 95

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
 100 105 110

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro
 115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140

Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met
 145 150 155 160

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<220>
<221> CDS
<222> (1) .. (666)
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<400> 44																	
atg	gtg	agt	gtg	atc	gct	aaa	caa	atg	acc	tac	aag	gtt	tat	atg	tca	48	
Met	Val	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met	Ser		
1				5				10						15			
ggc	acg	gtc	aat	gga	cac	tac	ttt	gag	gtc	gaa	ggc	gat	gga	aaa	gga	96	
Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	Gly		
		20						25						30			
aag	cct	tac	gag	gga	gag	cag	aca	gta	aag	ctc	act	gtc	acc	aag	ggg	144	
Lys	Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	Gly		
		35				40						45					
gga	cct	ctg	cca	ttt	gct	tgg	gat	att	tta	tca	cca	ctg	atg	tgt	tac	192	
Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Met	Cys	Tyr		
50						55						60					
gga	agc	ata	cca	ttc	acc	aag	tac	cct	gaa	gac	atc	cct	gat	tat	gta	240	
Gly	Ser	Ile	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Val		
65					70				75						80		
aag	cag	tca	ttc	cct	gag	gga	tat	aca	tgg	gag	agg	acc	atg	aac	ttt	288	
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Thr	Met	Asn	Phe		
				85				90						95			
gaa	gat	ggg	gca	gtg	tgt	act	gtc	agc	aat	gat	tcc	agc	atc	caa	ggc	336	
Glu	Asp	Gly	Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln	Gly		
		100						105						110			
aac	tgt	ttc	atc	tac	aat	gtc	aaa	atc	tct	ggg	acg	aac	ttt	cct	ccc	384	
Asn	Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Pro	Pro		
		115				120						125					

aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140
 gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat atg 480
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met
 145 150 155 160
 gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct 528
 Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
 165 170 175
 act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat att 576
 Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile
 180 185 190
 gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624
 Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205
 gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tga 669
 Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 45
 <211> 255
 <212> PRT
 <213> Montipora. sp

<400> 45
 Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
 1 5 10 15
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30
 Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45
 Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln
 85 90 95
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
 115 120 125
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140

Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro
 145 150 155 160
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
 165 170 175
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
 180 185 190
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys
 195 200 205
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu
 210 215 220
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
 225 230 235 240
 Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 245 250 255

<210> 46
 <211> 765
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1)..(765)

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 Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
 1 5 10 15
 ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30
 ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144
 Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45
 tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192
 Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60
 gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80
 ggt gga cct ctg cca ttt gct tgg gat att tta tca cca cag ttc cag 288
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln
 85 90 95

tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110
 ttc aag cag tca ttc cct gag gga tat aca tgg gag agg agc atg aac 384
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
 115 120 125
 ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140
 ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct 480
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro
 145 150 155 160
 ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc 528
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
 165 170 175
 act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
 180 185 190
 atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys
 195 200 205
 tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag 672
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu
 210 215 220
 att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
 225 230 235 240
 gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 765
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Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45

Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60

Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Leu Gln
 85 90 95
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
 115 120 125
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro
 145 150 155 160
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
 165 170 175
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
 180 185 190
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys
 195 200 205
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu
 210 215 220
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
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 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg	144
Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met	
35 40 45	
tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa	192
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys	
50 55 60	
gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag	240
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys	
65 70 75 80	
ggg gga cct ctg cca ttt gct tgg gat att tta tca cca cag ctt cag	288
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Leu Gln	
85 90 95	
tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat	336
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr	
100 105 110	
ttc aag cag tca ttc cct gag gga tat aca tgg gag agg agc atg aac	384
Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn	
115 120 125	
ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa	432
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln	
130 135 140	
ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct	480
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro	
145 150 155 160	
ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc	528
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser	
165 170 175	
act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat	576
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr	
180 185 190	
atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa	624
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys	
195 200 205	
tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag	672
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu	
210 215 220	
att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct	720
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser	
225 230 235 240	
gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt	765
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Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
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Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
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Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
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Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
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Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
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Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
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Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
				165					170					175	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
			180					185					190		
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
		195					200					205			
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
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Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
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Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Val	Asp	Gly	Thr
				245					250					255	
Ala	Gly	Pro	Leu	Tyr	Asp	Glu	Val	Asp	Lys	Asp	Pro	Met	Ala	Ser	Ser
			260					265					270		

Glu	Asp	Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Lys	Val	Arg	Met	Glu	Gly	
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Ser	Val	Asn	Gly	His	Glu	Phe	Glu	Ile	Glu	Gly	Glu	Gly	Glu	Gly	Arg	
	290					295					300					
Pro	Tyr	Glu	Gly	Thr	Gln	Thr	Ala	Lys	Leu	Lys	Val	Thr	Lys	Gly	Gly	
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Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Gln	Phe	Gln	Tyr	Gly	
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Ser	Lys	Ala	Tyr	Val	Lys	His	Pro	Ala	Asp	Ile	Pro	Asp	Tyr	Leu	Lys	
		340						345					350			
Leu	Ser	Phe	Pro	Glu	Gly	Phe	Lys	Trp	Glu	Arg	Val	Met	Asn	Phe	Glu	
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Asp	Gly	Gly	Val	Val	Thr	Val	Thr	Gln	Asp	Ser	Ser	Leu	Gln	Asp	Gly	
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Glu	Phe	Ile	Tyr	Lys	Val	Lys	Leu	Arg	Gly	Thr	Asn	Phe	Pro	Ser	Asp	
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Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Met	Gly	Trp	Glu	Ala	Ser	Thr	Glu	
			405						410					415		
Arg	Met	Tyr	Pro	Glu	Asp	Gly	Ala	Leu	Lys	Gly	Glu	Ile	Lys	Met	Arg	
			420					425					430			
Leu	Lys	Leu	Lys	Asp	Gly	Gly	His	Tyr	Asp	Ala	Glu	Val	Lys	Thr	Thr	
	435						440					445				
Tyr	Met	Ala	Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly	Ala	Tyr	Lys	Thr	Asp	
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Ile	Lys	Leu	Asp	Ile	Thr	Ser	His	Asn	Glu	Asp	Tyr	Thr	Ile	Val	Glu	
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Gln	Tyr	Glu	Arg	Ala	Glu	Gly	Arg	His	Ser	Thr	Gly	Ala	Ser	Gly	Leu	
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Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Val	Asp	Gly	Thr	Ala	Gly	
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Pro	Leu	Tyr	Asp	Glu	Val	Gly	Lys	Asp	Pro	Met	Ala	Ser	Ser	Glu	Asp	
	515						520					525				
Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Lys	Val	Arg	Met	Glu	Gly	Ser	Val	
	530					535					540					
Asn	Gly	His	Glu	Phe	Glu	Ile	Glu	Gly	Glu	Gly	Glu	Gly	Arg	Pro	Tyr	
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Glu	Gly	Thr	Gln	Thr	Ala	Lys	Leu	Lys	Val	Thr	Lys	Gly	Gly	Pro	Leu	
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 Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser
 595 600 605
 Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly
 610 615 620
 Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe
 625 630 635 640
 Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro
 645 650 655
 Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met
 660 665 670
 Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys
 675 680 685
 Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met
 690 695 700
 Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys
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 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
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 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag	240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
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cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc	720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
225 230 235 240	
gga ctc aga tct cga gct caa gct tgc aat tct gca gtc gac ggt acc	768
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr	
245 250 255	
gcg ggc ccg ctg tac gac gaa gtc gat aag gat ccg atg gcc tcc tcc	816
Ala Gly Pro Leu Tyr Asp Glu Val Asp Lys Asp Pro Met Ala Ser Ser	
260 265 270	

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Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly	
275 280 285	
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Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg	
290 295 300	
ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc	960
Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly	
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Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly	
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Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys	
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Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu	
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Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu	
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cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg	1296
Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg	
420 425 430	
ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc	1344
Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr	
435 440 445	
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Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp	
450 455 460	
atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa	1440
Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu	
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Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala Ser Gly Leu	
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Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly	
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ccg ctg tac gac gaa gtc ggt aag gat ccg atg gcc tcc tcc gag gac	1584
Pro Leu Tyr Asp Glu Val Gly Lys Asp Pro Met Ala Ser Ser Glu Asp	
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Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly Ser Val	
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aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc ccc tac	1680
Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr	
545 550 555 560	
gag ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg	1728
Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu	
565 570 575	
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Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys	
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Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser	
595 600 605	
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Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly	
610 615 620	
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Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe	
625 630 635 640	
atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc	1968
Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro	
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gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag cgg atg	2016
Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met	
660 665 670	
tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag	2064
Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys	
675 680 685	
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Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met	
690 695 700	
gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag	2160
Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys	
705 710 715 720	

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 35 40 45
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 50 55 60
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 65 70 75 80
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 85 90 95
 Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 100 105 110
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 115 120 125
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 130 135 140
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 145 150 155 160
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 165 170 175
 Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 180 185 190
 Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 195 200 205
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 210 215 220

Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	225	230	235	240
Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	245	250	255	
Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	260	265	270	
Ser	Ser	Ser	Glu	Leu	Ser	Gly	Asp	Glu	Val	Asp	Gly	Thr	Met	Val	Ser	275	280	285	
Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met	Ser	Gly	Thr	Val	290	295	300	
Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	Gly	Lys	Pro	Tyr	305	310	315	320
Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	Gly	Gly	Pro	Leu	325	330	335	
Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Phe	Gln	Tyr	Gly	Ser	Ile	340	345	350	
Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Val	Lys	Gln	Ser	355	360	365	
Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Thr	Met	Asn	Phe	Glu	Asp	Gly	370	375	380	
Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln	Gly	Asn	Cys	Phe	385	390	395	400
Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Pro	Pro	Asn	Gly	Pro	405	410	415	
Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser	Thr	Glu	Arg	Leu	420	425	430	
Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr	Met	Ala	Leu	Lys	435	440	445	
Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys	Ser	Thr	Tyr	Lys	450	455	460	
Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Tyr	His	Tyr	Ile	Asp	Arg	Lys	465	470	475	480
Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser	Val	Glu	Gln	Cys	485	490	495	
Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly						500	505		

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 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

ccc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc 144
 Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 35 40 45

ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc 192
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 50 55 60

ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 240
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 65 70 75 80

atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 288
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 85 90 95

acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 336
 Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 100 105 110

aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 384
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 115 120 125

gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc 432
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 130 135 140

gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag 480
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 145 150 155 160

ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag 528
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 165 170 175

tac aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag 576
 Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 180 185 190

aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc	624
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly	
195 200 205	
agc gtg cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac	672
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
210 215 220	
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Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala	
225 230 235 240	
ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	768
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
245 250 255	
ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	816
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
260 265 270	
tcc tcg tcc gag ctg agc gga gat gag gtc gat ggt acc atg gtg agt	864
Ser Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser	
275 280 285	
gtg atc gct aaa caa atg acc tac aag gtt tat atg tca ggc acg gtc	912
Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val	
290 295 300	
aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct tac	960
Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr	
305 310 315 320	
gag gga gag cag aca gta aag ctc act gtc acc aag ggt gga cct ctg	1008
Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro Leu	
325 330 335	
cca ttt gct tgg gat att tta tca cca ctg ttt cag tac gga agc ata	1056
Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr Gly Ser Ile	
340 345 350	
cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag cag tca	1104
Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser	
355 360 365	
ttc cct gag gga tat aca tgg gag agg acc atg aac ttt gaa gat ggt	1152
Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe Glu Asp Gly	
370 375 380	
gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt ttc	1200
Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe	
385 390 395 400	
atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc aat gga cct	1248
Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro Asn Gly Pro	
405 410 415	

gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act gag cgt ctc 1296
 Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr Glu Arg Leu
 420 425 430

ttt gca cga gat gga atg ctg ata gga aac gat tat atg gct ctg aag 1344
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 435 440 445

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 450 455 460

gca aag aag cct gtg agg atg cca ggg tat cac tat att gac cgc aaa 1440
 Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile Asp Arg Lys
 465 470 475 480

ctg gat gta acc agt cac aac agg gat tac aca tct gtt gag cag tgt 1488
 Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val Glu Gln Cys
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 <213> Montipora. sp

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Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45

Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60

Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80

Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln
 85 90 95

Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110

Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn
 115 120 125

Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140

Gly	Asn	Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Pro	145	150	155	160
Pro	Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser	165	170	175	
Thr	Glu	Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr	180	185	190	
Met	Ala	Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys	195	200	205	
Ser	Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Tyr	His	Tyr	210	215	220	
Ile	Asp	Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser	225	230	235	240
Val	Glu	Gln	Cys	Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly	Ser	245	250	255	
Ser	Ser	Glu	Leu	Ser	Gly	Asp	Glu	Val	Asp	Gly	Thr	Met	Val	Ser	Lys	260	265	270	
Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	275	280	285	
Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	290	295	300	
Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	305	310	315	320
Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Trp	Gly	325	330	335	
Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	340	345	350	
Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	355	360	365	
Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	370	375	380	
Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	385	390	395	400
Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	405	410	415	
His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala	420	425	430	
Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	435	440	445	

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 450 455 460
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 465 470 475 480
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 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30
 ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144
 Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45
 tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192
 Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60
 gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80
 ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt cag 288
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln
 85 90 95
 tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110
 gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac 384
 Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn
 115 120 125

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Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln	
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ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct	480
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro	
145 150 155 160	
ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc	528
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser	
165 170 175	
act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat	576
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr	
180 185 190	
atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa	624
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys	
195 200 205	
tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat	672
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr	
210 215 220	
att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct	720
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser	
225 230 235 240	
gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tcc	768
Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly Ser	
245 250 255	
tcg tcc gag ctc agc gga gat gag gtc gat ggt acc atg gtg agc aag	816
Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser Lys	
260 265 270	
ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac	864
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp	
275 280 285	
ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc	912
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly	
290 295 300	
gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc	960
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly	
305 310 315 320	
aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc	1008
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly	
325 330 335	
gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc	1056
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe	
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 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 355 360 365
 ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag 1152
 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
 370 375 380
 ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 1200
 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
 385 390 395 400
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 1248
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
 405 410 415
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 1296
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
 420 425 430
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 1344
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 435 440 445
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 1392
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 450 455 460
 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 1440
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 465 470 475 480
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 1488
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
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 Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 35 40 45

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser
 50 55 60
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
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 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 85 90 95
 Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 100 105 110
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 115 120 125
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 130 135 140
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 145 150 155 160
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 165 170 175
 Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 180 185 190
 Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 195 200 205
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 210 215 220
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 225 230 235 240
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 245 250 255
 Phe Val Thr Ala Ala Arg Met His Asp Gln Leu Thr Glu Glu Gln Ile
 260 265 270
 Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly
 275 280 285
 Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln
 290 295 300
 Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala
 305 310 315 320
 Asp Gly Asn Gly Thr Ile Tyr Phe Pro Glu Phe Leu Thr Met Met Ala
 325 330 335
 Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe
 340 345 350

Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu
 355 360 365

Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val
 370 375 380

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Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys
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 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

ccc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc 144
 Pro Met Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile
 35 40 45

ctg gtc gag ctg gac ggc gac gta aac ggc cac agg ttc agc gtg tcc 192
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser
 50 55 60

ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 240
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 65 70 75 80

atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 288
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 85 90 95

acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 336
 Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 100 105 110

aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 384
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 115 120 125

gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc	432
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala	
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gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag	480
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys	
145 150 155 160	
ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag	528
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu	
165 170 175	
tac aac tat atc agc cac aac gtc tat atc acc gcc gac aag cag aag	576
Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
180 185 190	
aac ggc atc aag gcc cac ttc aag atc cgc cac aac atc gag gac ggc	624
Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly	
195 200 205	
agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	672
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
210 215 220	
ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc	720
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala	
225 230 235 240	
ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	768
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
245 250 255	
ttc gtg acc gcc gcc cgc atg cat gac caa ctg aca gaa gag cag att	816
Phe Val Thr Ala Ala Arg Met His Asp Gln Leu Thr Glu Glu Gln Ile	
260 265 270	
gca gag ttc aaa gaa gcc ttc tca tta ttc gac aag gat ggg gac ggc	864
Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly	
275 280 285	
acc atc acc aca aag gaa ctt ggc acc gtt atg agg tcg ctt gga caa	912
Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln	
290 295 300	
aac cca acg gaa gca gaa ttg cag gat atg atc aat gaa gtc gat gct	960
Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala	
305 310 315 320	
gat ggc aat gga acg att tac ttt cct gaa ttt ctt act atg atg gct	1008
Asp Gly Asn Gly Thr Ile Tyr Phe Pro Glu Phe Leu Thr Met Met Ala	
325 330 335	
aga aaa atg aag gac aca gac agc gaa gag gaa atc cga gaa gca ttc	1056
Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe	
340 345 350	

cgt	gtt	ttt	gac	aag	gat	ggg	aac	ggc	tac	atc	agc	gct	gct	gaa	tta	1104
Arg	Val	Phe	Asp	Lys	Asp	Gly	Asn	Gly	Tyr	Ile	Ser	Ala	Ala	Glu	Leu	
		355					360					365				
cgt	cac	gtc	atg	aca	aac	ctc	ggg	gag	aag	tta	aca	gat	gaa	gaa	gtt	1152
Arg	His	Val	Met	Thr	Asn	Leu	Gly	Glu	Lys	Leu	Thr	Asp	Glu	Glu	Val	
		370				375					380					
gat	gaa	atg	ata	agg	gaa	gca	gat	atc	gat	ggg	gat	ggc	caa	gta	aac	1200
Asp	Glu	Met	Ile	Arg	Glu	Ala	Asp	Ile	Asp	Gly	Asp	Gly	Gln	Val	Asn	
385					390					395					400	
tat	gaa	gag	ttt	gta	caa	atg	atg	aca	gca	aag						1233
Tyr	Glu	Glu	Phe	Val	Gln	Met	Met	Thr	Ala	Lys						
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<213> Montipora. sp
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1				5					10					15			
Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Lys	Asp		
			20					25						30			
Pro	Lys	Arg	Arg	Trp	Lys	Lys	Asn	Phe	Ile	Ala	Val	Ser	Ala	Ala	Asn		
		35					40					45					
Arg	Phe	Lys	Lys	Ile	Ser	Ser	Ser	Gly	Ala	Leu	Gly	Gly	Gly	Gly	Ser		
	50					55					60						
Glu	Leu	Met	Val	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr		
65					70					75					80		
Met	Ser	Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly		
				85					90					95			
Lys	Gly	Lys	Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr		
			100					105						110			
Lys	Gly	Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Phe		
		115					120					125					
Gln	Tyr	Gly	Ser	Ile	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp		
	130					135					140						
Tyr	Val	Lys	Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Thr	Met		
145					150					155					160		
Asn	Phe	Glu	Asp	Gly	Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile		
				165					170						175		

Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe
 180 185 190

Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro
 195 200 205

Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp
 210 215 220

Tyr Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe
 225 230 235 240

Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His
 245 250 255

Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr
 260 265 270

Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 275 280 285

<210> 58
 <211> 864
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1)..(864)

<400> 58
 atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act 48
 Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
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ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

ccc aag agg cgc tgg aag aaa aac ttc att gcc gtc agc gct gcc aac 144
 Pro Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn
 35 40 45

cgg ttc aag aag atc tcc agc tcc ggg gca ctg gga ggt gga ggt agt 192
 Arg Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu Gly Gly Gly Gly Ser
 50 55 60

gag ctc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat 240
 Glu Leu Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr
 65 70 75 80

atg tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga 288
 Met Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly
 85 90 95

aaa gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc	336
Lys Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr	
100 105 110	
aag ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt	384
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe	
115 120 125	
cag tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat	432
Gln Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp	
130 135 140	
tat gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg	480
Tyr Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met	
145 150 155 160	
aac ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc	528
Asn Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile	
165 170 175	
caa ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt	576
Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe	
180 185 190	
cct ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc	624
Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro	
195 200 205	
agc act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat	672
Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp	
210 215 220	
tat atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt	720
Tyr Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe	
225 230 235 240	
aaa tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac	768
Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His	
245 250 255	
tat att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca	816
Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr	
260 265 270	
tct gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt	864
Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly	
275 280 285	

<210> 59

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 59
ccagagatga agatgaggta ctacatggac ggc 33

<210> 60
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 60
catgagttca caattgaagg tgaaggc 27

<210> 61
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 61
gaaggcacag gcagacctta cgaggga 27

<210> 62
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 62
ccaatgcctt tcgcgtttga cttagtg 27

<210> 63
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 63
ttagtgtcac acgtgttctg ttacggc 27

<210> 64
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 64
 gaaaggtcgt tggagttcga agatggt

27

<210> 65
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 65
 gaagatgggtg ggtccgcttc agtcagtgcg

30

<210> 66
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 66
 agccttagag gaaacacctt ctaccacaaa tcca

34

<210> 67
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 67
 caaatccaaa ttactgggg ttaactttcc tg

32

<210> 68
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 68
 gccgatggtc ctatcatgca aaaccaaagt 30

 <210> 69
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 69
 gccgatggtc ctatcatgca aaaccaaagt gttgattggg agcca 45

 <210> 70
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 70
 gagaaaatta ctgccagcga cggagttctg aag 33

 <210> 71
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 71
 gatgttacga tgtacctaaa acttgaagga ggcggcaatc ac 42

 <210> 72
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 72
 cttaaaatgc caggaagcca ttacatcagc catcgctcg tcagg 45

<210> 73
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 73
 gatgcagtag ctcattccct cgagcaccac cacc 34

<210> 74
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 74
 gaaggrtgyg tcaayggrca y 21

<210> 75
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 75
 acvggdccat ydgvaagaaa rtt 23

<210> 76
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (24)..(25)
 <223> inosine

<220>
 <221> modified_base
 <222> (29)..(30)
 <223> inosine

<220>
 <221> modified_base
 <222> (34)..(35)
 <223> inosine

<400> 76
 ggccacgcgt cgactagtagt gggnnngggnn gggnnng

36

<210> 77
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 77
 ctcaggggaat gactgcttta cat

23

<210> 78
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 78
 ggccacgcgt cgactagtagt

20

<210> 79
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 79
 gtcttcaggg tacttggtga

20

<210> 80
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 80
 atgtaaagca gtcattccct gag 23

<210> 81
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 81
 cccggatccg accatggcta ccttggttaa aga 33

<210> 82
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 82
 Asp Glu Val Asp
 1

<210> 83
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 83
 Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys
 1 5 10

<210> 84
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 84

Gly Gly Ser Gly Gly Asp Glu Val Asp Gly Thr Gly Gly Ser
1 5 10